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           Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
           Shibahara,T., Nakahara,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE      NEDO human cDNA sequencing project
JOURNAL    Unpublished
REFERENCE  2  (bases 1 to 2383)
AUTHORS    Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
           Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE      Direct Submission
JOURNAL    Submitted (29-AUG-2000) Sunio Sugano, Institute of Medical Science,
           University of Tokyo, Laboratory of Genome Structure Analysis, Human
           Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
           Japan (E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
           Fax:81-3-5449-5416)
COMMENT    NEDO human cDNA sequencing project supported by Ministry of
           International Trade and Industry of Japan; cDNA full insert
           sequencing: Research Association for Biotechnology; cDNA library
           construction, 5'- & 3'-end one pass sequencing: Department of
           Virology and Human Genome Center Institute of Medical Science,
           University of Tokyo (partly supported by Science and Technology
           Agency).
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="HEP16084"
                     /cell_line="HepG2"
                     /cell_type="hepatoma"
                     /clone_lib="HEP"
                     /note="cloning vector pME18SFL3"
BASE COUNT      581 a    574 c    651 g    577 t
ORIGIN

Query Match         99.3%;  Score 2357.2;  DB 9;  Length 2383;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 2370;  Conservative  0;  Mismatches  3;  Indels  1;  Gaps  1;
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Db      1 CTTTTCTCTTGTTGAGTGCAAATGGAGAACAGCTGCTCACGCGTCGTCTCGACATCAGC 60

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Db  49704 AGGGTCGAGCTGTTCCTGATGTTTATCGGAGACTGGGATCAAAGCTATCCAGGTCATAAA 49763

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Qy   2161 ATTGTAGAAATAGCTTAACCCTTTCATTTACCAACGTGGAAATTGAAGCCCAGGGAAGGG 2220
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Db  50843 AAGGGACCGGTCGTGGAAGGGAGAGCCATCAGCAGAAAGAGACCCTGAGATCTTCGCCTG 50902

Qy   2281 GGATTCCCAGGAAGTCCAGCCCGAGCTGATTCACAGAACAAATGCATGCAAACCTTGCTA 2340
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Qy   2341 TCAATAAATTACACATGCACTTACGTAAAACACAT 2375
          |||||||||||||||||||||||||||||||||||
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RESULT 3
AK025743

LOCUS   AK025743   2383 bp   mRNA   linear   PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA: FLJ22090 fis, clone HEP16084.
ACCESSION   AK025743
VERSION   AK025743.1 GI:10438355
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
            clone:HEP16084.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
  AUTHORS   Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,

Sequence Match Listing
for SEQ ID NO:5

RESULT 3
US-09-385-982-202/c
Sequence 202, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 202
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(620)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-202

Query Match   0.8%; Score 18; DB 4; Length 620;
Best Local Similarity   100.0%; Pred. No. 37;
Matches   18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   628 ACCACCCCATCATCACC 645
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Db   349 ACCACCCCATCATCACC 332

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RESULT 4
AP000067
LOCUS       AP000067   100000 bp   DNA   linear   PRI 25-MAY-2002
DEFINITION  Homo sapiens genomic DNA, chromosome 8p11.2, senescence gene
            region, section 3/19.
ACCESSION   AP000067
VERSION     AP000067.1  GI:4579988
KEYWORDS    .
SOURCE      Homo sapiens DNA.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Isomura,M., Ikegawa,S., Kinjo,T. and Nakamura,Y.
TITLE       DNA sequence analysis of a 1.9-Mb region on chromosome 8p11.2
JOURNAL     Published Only in Database (1999)
REFERENCE   2  (bases 1 to 100000)
AUTHORS     Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
TITLE       Direct Submission
JOURNAL     Submitted (12-FEB-1999) Mika Hirakawa, Japan Science and Technology
            Corporation (JST), Advanced Database Department; 5-3, Yonban-cho,
            Chiyoda-ku, Tokyo 102-0028, Japan (E-mail:mika@tokyo.jst.go.jp,
```
```
            Tel:81-3-5214-8491, Fax:81-3-5214-8470)
COMMENT     This sequence is conducted by Japanese Foundation for Cancer
            Research as a JST sequencing Team.
            Principal Investigator: Yusuke Nakamura, Ph.D
            Phone:+81-3-5449-5372, Fax:+81-3-5449-5433,
            yusuke@hgc.ims.u-tokyo.ac.jp
            The sequence is submitted by Human Genome Sequencing in AllS
            project of JST.
            Japan Science and Technology Corporation (JST)
            5-3, Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan
            For further infomation about this sequence, please visit our
            sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/cop.
            html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
FEATURES             Location/Qualifiers
     source          1..100000
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                     /chromosome="8"
                     /map="8p11.2"
     STS             66183..66318
                     /standard_name="D8S571"
                     /note="1264/895;The location is between each flanking site
                     of PCR primers."
                     /db_xref="GDB:214930"
BASE COUNT    24961 a  22749 c  24235 g  28036 t     19 others
ORIGIN
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Query Match     99.2%;  Score 2356.6;  DB 9;  Length 100000;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 2370;  Conservative   0;  Mismatches   4;  Indels   1;  Gaps   1;

Qy          1 CTTTTCTCTTGTTGAGTGCAAAATGGAGAACAGCTTGCTCACGCTCGTCGTCTGACATCAGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48624 CTTTTCTCTTGTTGAGTGCAAAATGGAGAACAGCTTGCTCACGCTCGTCGTCTGACATCAGC 48683

Qy         61 TATTTCTCAGGATGACCCTGCGAGACAGCCCAGGGTCATTAGACCCAAATTTGGTTCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48684 TATTTCTCAGGATGACCCTGCGAGACAGGCCAGGGTCATTAGACCCAAATTTGGTTCTCAG 48743

Qy        121 CAAATATGTGTTTTATTCCTGCATGCGTGGGCCACAGGCTGGGTTTCTTGGGTTCTCAAT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48744 CAAATATGTGTTTTATTCCTGCATGCGTGGGCCACAGGCTGGGTTTCTTGGGTTCTCAAT 48803

Qy        181 AGCTGCAGGTTTATTAGGGTGTCTCTTTTAGATGGATGGATGTATAGTTCCCGGATGTCTATAGAA 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48804 AGCTGCAGGTTTATTAGGGTGTCTCTTTTAGATGGATGTATAGTTCCCGGATGTCTATAGAA 48863

Qy        241 CACTCCGGACCCCGAGGAGTGAAGACTCTGCCTGTCCGGACTTGCTTGAAGATCCTTC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48864 CACTCCGGACCCCGAGGAGTGAAGACTCTGCCTGTCCGGACTTGCTTGAAGATCCTTC 48923

Qy        301 TCCACCTCCCCATGGGCAGAAGTTGCTTCACGAGGGGGAACAGTTTATGGGATGTGGCTGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48924 TCCACCTCCCCATGGGCAGAAGTTGCTTCACGAGGGGGAACAGTTTATGGGATGTGGCTGA 48983

Qy        361 GACCTTAAACTTGAGGCACACCCATCTGAGGTGGCATCCAGAGAGAGACTGGCTGGCCCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49043 GACCTTAAACTTGAGGCACACCCATCTGAGGTGGCATCCAGAGAGAGACTGGCTGGCCCTC 49043

Qy        421 CTTCACCTTGGATGTAGTGTCTGTTTCTAGGATCTCTTTTTCAATCAGCAAAAACAGGGGATG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49044 CTTCACCTTGGATGTAGTGTCGTTTCTAGGATCTCTTTTTCAATCAGCAAAAACAGGGGATG 49103

Qy        481 TTCCAAGAGGGTGTGGAATTCCCTGCCATCCCACATGGTCAAGTGGGAGGGGACGCGGGAAAAA 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49104 TCCCAAGAGGGTGTGGAATTCCCTGCCATCCACATGGTCAAGTGGGAGGGGACGGGAAAAA 49163

Qy        541 GCTATGAAAGGGTTTGTGACCACACAGACTCTCTGGCCCCCGTCCTTTTGGAAAGAGAGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49164 GCTATGAAAGGGTTTGTGACCACACAGACTCTCTGGCCCCCGTCCTTTTGGAAAGAGAGA 49223

Qy        601 CAGGGATGAAAATAATCAAGCAATTAACCACCCCATCATCACCAGAACAACAGTATC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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